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### Proposed structure for the zinc-binding domains from transcription factor IIIA and related proteins.

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Several proteins, including the gene regulatory protein transcription factor IIIA, have been shown to contain tandem repeats of sequences of approximately equal to 30 amino acids that are believed to form structural domains around bound zinc ions ("zinc fingers"). The consensus sequence for these repeats is (Phe, Tyr)-Xaa-Cys-(Xaa)<sub>2</sub> or 4-Cys-(Xaa)<sub>3</sub>-Phe-(Xaa)<sub>5</sub>-Leu-(Xaa)<sub>2</sub>-His-(Xaa)<sub>3</sub>-His-(Xaa)<sub>5</sub>, where Xaa is any amino acid. Comparisons with metalloproteins with known structures have allowed the development of a detailed three-dimensional model for these domains consisting of an antiparallel beta-sheet followed by an alpha-helix. The proposed structure provides a basis for understanding the detailed roles of the conserved residues and allows construction of a model for the interaction of these proteins with nucleic acids in which the proteins wrap around the nucleic acids in the major groove.

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